AMENDMENTS TO THE SPECIFICATION:

Please amend the indicated paragraphs of the specification in accordance with the amendments indicated below.

Page 1:First full paragraph, amend the title as indicated below:

A ~~NOVEL~~ METHOD FOR PREDICTING THE SPATIAL-ARRANGEMENT TOPOLOGY OF AN AMINO ACID SEQUENCE USING FREE ENERGY COMBINED WITH SECONDARY STRUCTURAL INFORMATION

Pages 7-9: Paragraph bridging pages 7-8, amend as indicated below:

Further, the invention of this application may comprise the following steps: ~~inputting an amino acid sequence of a protein,~~

A. inputting an amino acid sequence of a protein,

B. preparing information on the secondary structure of the said amino acid sequence by way of at least one theoretical or experimental estimate,

C. applying the CLE method to the said amino acid sequence and secondary structure information to evaluate the free energy of a combinatorial number of β-strand and α-helix arrangements as rapidly as polynomial time: $c(n-1)(n+1)$ wherein c is a constant and n is the number of secondary structure elements found in the said amino acid in ~~2A~~ A and prepared in B ~~2B~~,

D. applying the CLE method in conjunction with other thermodynamic potentials that approximate hydrophobic,

electrostatic and polar interactions, but not limited to these aforementioned thermodynamic potentials stated herein, in a thermodynamic calculation to account for both short and long range folding interactions and predict a minimum free energy and corresponding topology of the said amino acid sequence,

E. applying the CLE method to predict the global folding kinetics of the said amino acid sequence, and

F. storing the information in a data file or in other form of digital memory.

Pages 11-12: Paragraph bridging pages 11-12, amend as indicated below:

Here, the total CLE contribution to the free energy (ΔG_{cle}) can be calculated by equation (2):

$$\Delta G_{cle} = \Delta G_{\xi}^{o} + \sum_{all\_bonds(i,j)} \Delta G_{ij} + \sum_{i',j'} f_{i'j'}(\xi) \qquad (2)$$

wherein, ΔG_{ij} is defined in equation (1), i' and j' are indices specifying two secondary structure elements (α-helices or β-strands) that are joined together by the corresponding set of bonds i and j, $f_{i'j'}(\xi)$ is a positive definite penalty function used to enforce topology constraints on the minimum allowed sequence length of a loop connecting two elements of secondary structure i' j' and is a function of the persistence length ξ, and ΔG_{ξ}^{o} is a renormalization correction and is an integral function of ξ as shown by equation (3):

$$\Delta G_{\xi}^{o} = \frac{(\gamma + 1/2)Nk_B T}{D\xi} \int_{+1}^{\xi} \left(\frac{\ln(x)}{(1-x)} + 1 \right) dx \qquad (3)$$

wherein, ξ, γ, k_B, and T mean the same as defined in the disclosure ~~claim 7~~, N indicates the number of amino acids in the said sequence, D is the dimensionality of the system, the limits in the integral $(1 \rightarrow \xi)$ indicate the change in the number of degrees of freedom from an individual amino acid reside to a cluster of ξ amino acids treated as a group (where ξ>1 amino acid and ξ need not be an integer) and x is dummy variable in the integral substituting for ξ.